

Amendment and Response

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For: DNA REPAIR POLYPEPTIDES AND METHODS OF USE

amino acids, although the amino acids in each sequence must nonetheless remain in their proper order. A candidate amino acid sequence is the amino acid sequence being compared to an amino acid sequence present in SEQ ID NO:41, SEQ ID NO:42, or SEQ ID NO:43. A candidate amino acid sequence can be isolated from a microbe or a microbe harboring a virus, or can be produced using recombinant techniques, or chemically or enzymatically synthesized. Preferably, two amino acid sequences (i.e., the candidate amino acid sequence and the amino acid sequence present in SEQ ID NO:41, SEQ ID NO:42, or SEQ ID NO:43) are compared using the Blastp program of the BLAST 2 search algorithm, as described by Tatusova, et al. (*FEMS Microbiol Lett* 1999, 174:247-250), and available on the worldwide web at ncbi.nlm.nih.gov/gorf/b12.html. Preferably, the default values for all BLAST 2 search parameters are used, including matrix = BLOSUM62; open gap penalty = 11, extension gap penalty = 1, gap x_dropoff = 50, expect = 10, wordsize = 3, and filter on. In the comparison of two amino acid sequences using the BLAST search algorithm, amino acid identity is referred to as "identities." Preferably, a polypeptide having pyrimidine glycolase activity has an amino acid sequence having, in increasing order of preference, at least about 15 % amino acid identity, at least about 30 % amino acid identity, at least about 40 % amino acid identity, at least about 50 % amino acid identity, and most preferably, at least about 60 % amino acid identity to SEQ ID NO:41, SEQ ID NO:42, or SEQ ID NO:43.

In the Claims

Please amend claims 1, 3, 9-12 and 21-40. The amended claims are provided below in clean form. Per 37 C.F.R. §1.121, amended claims are also shown in Appendix A with notations to indicate changes made (for convenience, all pending claims, including those added hereby, are provided in Appendix A).

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1. [TWICE AMENDED] An isolated polypeptide comprising: